

## **I. AMENDMENT**

### **Amendments to the Specification:**

Please replace the paragraph beginning on page 14, line 14, with the following amended paragraph:

Identity is calculated according to methods known in the art. Sequence identity is most preferably assessed by the BLAST version 2.1 program advanced search (parameters as above). BLAST is a series of programs that are available online at <http://www.ncbi.nlm.nih.gov/BLAST>. The advanced BLAST search (<http://www.ncbi.nlm.nih.gov/blast/blast.cgi?Jform=1>) is set to default parameters. (i.e. Matrix BLOSUM62; Gap existence cost 11; Per residue gap cost 1; Lambda ratio 0.85 default).